

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 15:21:24 ; Search time 2494.08 seconds  
(without alignments)  
12850.800 Million cell updates/sec

Title: US-09-625-573-3

Perfect score: 1979

Sequence: 1 CAGGACTGCCTGAGACAAGC.....ATATGCAATATAAAATTTAG 1979

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469.8	23.7	807	13	BI764263
2	469	23.7	469	17	B84215
3	357.6	18.1	487	10	BE656336
4	326.2	16.5	542	9	AA547303
5	296.4	15.0	480	10	AA657263
6	292.6	14.8	447	9	AA671573

7	289	14.6	1074	14	BM917063
8	284.8	14.4	452	9	AI851510
9	276.6	14.0	907	9	AL552677
10	249.8	12.6	789	12	BG205056
11	247.8	12.5	341	17	AQ066245
12	239.4	12.1	869	12	BF119225
13	236.4	11.9	876	13	BI906283
14	235.2	11.9	884	12	BG182330
15	230	11.6	230	12	BF171452
16	220.8	11.2	952	14	BM917763
17	216.8	11.0	745	12	BG204024
18	214.6	10.8	1167	14	BQ053936
19	198.6	10.0	650	10	BB630138
20	197	10.0	672	10	BB638766
21	196.2	9.9	568	12	BF193051
22	189	9.6	780	13	BI908127
23	186.8	9.4	551	12	BF081124
24	181	9.1	863	13	BI661279
25	180.6	9.1	669	13	BI393893
26	179.4	9.1	533	12	BF193021
27	177.2	9.0	639	10	BB629533
28	175.2	8.9	723	14	BM951933
29	173.6	8.8	965	14	BQ944555
30	172.2	8.7	934	12	BG460984
31	169.2	8.5	787	9	AU080004
32	168.8	8.5	3005	11	AK019478
33	163.8	8.3	936	12	BF119806
34	153.2	7.7	665	10	BB628567
35	151.8	7.7	662	10	BB644135
36	151.6	7.7	600	13	BI987229
37	151.6	7.7	646	10	BB615654
38	147.2	7.4	867	13	BI106339
39	146.4	7.4	2111	11	AK007808
40	145.4	7.3	319	14	BM734515
41	141.2	7.1	574	17	AQ461727
42	140.6	7.1	804	13	BI685810
43	139.6	7.1	427	12	BF081123
44	138.2	7.0	668	10	BB645326
45	138	7.0	770	9	AJ452673

#### ALIGNMENTS

RESULT 1  
BI764263  
LOCUS  
DEFINITION 603045953F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5186388 5', linear EST 25-SEP-2001  
ACCESSION BI764263  
VERSION BI764263.1 GI:15755841  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 807)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgaps-remail.nih.gov](mailto:cgaps-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11465 row: i column: 13  
High quality sequence stop: 805.  
Location/Qualifiers  
1. .807



Db 241 GGGAGCAGGAAGTCTCGCTCGTGTATATAAAGAGGAGCAGTTCATTGTTGTTATTA 300

QY 1194 AGGAGATAACAATCTGTATATAACAACAACACTTCAAGGGTTGTTGTAACAATAGAAACC 1253

Db 301 AGGAGATAACAATCTGTATATAACAACAACACTTCAAGGGTTGTTGTAACAATAGAAACC 360

QY 1254 TGTAAAGCAGGTGCCAGGAACCTCAGGCTGTGTGTACTATATACAGACTATGTACCCA 1313

Db 361 TGTAAAGCAGGTGCCAGGAACCTCAGGCTGTGTGTACTATATACAGACTATGTACCCA 420

QY 1314 ATGCATATCCACATGTCTCAGGGAATATCCAGAAAACCTGTGGGTA 1362

Db 421 ATGCATATCCACATGTCTCAGGGAATATCCAGAAAACCTGTGGGTA 469

RESULT 3

BE56336 487 bp mRNA linear EST 06-SEP-2000

LOCUS UI-M-BH0-aju-h-06-0-UI.r1 NIH.BMAP\_M.S1 Mus musculus cDNA clone

DEFINITION UI-M-BH0-aju-h-06-0-UI 5', mRNA sequence.

ACCESSION BE56336

VERSION BE56336

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

COMMENT Contact: Chin, H  
National Institute of Mental Health  
2001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mestr@mail.nih.gov

CDNA Library Preparation: M.B. Soares Lab Clone Distribution:  
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements

Seq primer: M13 Reverse.

Location/Qualifiers

1. .487

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UI-M-BH0-aju-h-06-0-UI"

/clone\_lib="NIH\_BMAP\_M.S1"

/dev\_stage="27-32 days"

/lab\_host="DH10B (Life Technologies)"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; The NIH\_BMAP\_M.S1 library is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 20,000 cDNA clones obtained from non-normalized and normalized libraries of these ten regions of the mouse brain."

BASE COUNT 115 a 115 c 103 g 154 t

ORIGIN

Query Match 18.1%; Score 357.6; DB 10; Length 487;

Best Local Similarity 85.3%; Pred. No. 7e-89;

Matches 399; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 151 TTGATTATGATTACGGTCTCCCTGTATATAAATTTTACGCTGAAGCAAAATTTGGGGCCCAAC 210

Db 19 TCGATTATGATTATGTCAGCACCTCGCCAAAATCAATGTGAACAATAATTCGGGCTCAGC 78

QY 211 TCTGCTCTCGCTCTACTCGCTGGTGTTCATCTTTTGGTTTGTGGGCAACATGCTGGTCG 270

Db 79 TCTGCTCTCGCTCTACTCGCTGGTGTTCATCTTTTGGTTTGTGGGTAACATGATGTCT 138

QY 271 TCTCATCTATATAAAGCTGAAAAGCTGAAGTGTCTGTGACTGACATTTACCTGCTCAACC 330

Db 139 TCTCATCTGTATGAAGTGTAAAAGCTGAAGAGCTGACTGATATCTACTGCTCAACC 198

QY 331 TGCCCATCTCTGATCTGCTTTTCTTATTAATCTCCCATTTGGGGTCTACTTGTGTCGAA 390

Db 199 TGCCCATCTCTGATCTGCTTTTCTTATTAATCTCCCATTTGGGGTCTACTTGTGTCGAA 258

QY 391 ATGAGTGGGTCTTTGGGAATGCAATGTGCAAAATTTTACAGGGCTGTATCATCATCGGTT 450

Db 259 ATGAGTGGGTCTTTGGGAATGCAATGTGTAAGTATTACAGGGCTCTATCATCATGGTT 318

QY 451 ATTTTGGGGAATCTTCTTCATCATCTCCTGACAAATCGATAGATACCTGGCTATTGTC 510

Db 319 ATTTTGGTGAATCTTCTTCATCATCTCCTGACAAATGTAGTACTTGGCTATTGTC 378

QY 511 ATGCTGTGTTGCTTTTAAAAGCCAGGAGCTCACCTTTGGGGTGGTGACAAAGTGTGATCA 570

Db 379 ATGCTGTGTTGCTTTTAAAAGTCCAGACGCTCAACTTTGGGGTGATAACAAGTGTAGTCA 438

QY 571 CTGTTGGTGGGTGCTGTTTGTCTCTGCCAGGAATCATCTTTTACTA 618

Db 439 CTGTTGGGTGGGTGCTGTTTGTCTCTGCCAGGAATCATCTTTTACTA 486

RESULT 4

AA547303 542 bp mRNA linear EST 05-AUG-1997

LOCUS vk28h04.r1 Soares\_mammary\_gland\_NbMMG Mus musculus cDNA clone

DEFINITION IMAGE:947959 5', similar to SW:CKR2.HUMAN P41597 MONOCYTE CHEMOATTRACTANT PROTEIN 1 RECEPTOR ;, mRNA sequence.

ACCESSION AA547303

VERSION AA547303.1 GI:2308594

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS 1 (bases 1 to 542)  
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Willson,R. and Waterston,R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:544815  
High quality sequence stop: 286.

FEATURES

source

1. .542

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:947959"

/clone\_lib="Soares\_mammary\_gland\_NbMMG"

/sex="male"

REFERENCE  
AUTHORS  
Bovidae: Bovinae: Bos.  
1 (bases 1 to 480)  
Smith,T.P.I., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,  
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,  
Pertege,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and  
Keeler,J.W.  
TITLE  
Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
JOURNAL  
Genome Res. 11(4), 626-630 (2001)

Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.

```

FEATURES
    source
        1. .480
            Location/Qualifiers
                Seq primer: ATTAGGTGACACTATAG.
                Plate: 100 row: 0 column: 13
                BACKWARD: GTTTCCTCAGTCACGACG
                FORWARD: AGGAACAGCTATGACCAT
            and "minmatch 12 options.
            PCR primers

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/note="Vector: pCMV SPORT6; Site\_1: NotI; Site\_2: SalI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary "

Query Match 15.0%; Score 296.4; DB 10; Length 480;  
Best Local Similarity 79.4%; Pred. No. 9.8e-72;

**Matches 381; Conservative 0; Mismatches 86; Indels 13; Gaps 2;**

540 GTCACCTTTGGGGTGGTGACAAAGTGTGATCACCTGGTTGGTGGCTGTGTTTGCTTCTGTC 599

1 GTCACCTTTGGGGCGGGCACAAGTGGTGACCTGGGTGGTGGCTGTGTTGGCTCTC 60

**C**

600 CCAGGAATCATCTTTACTAAATGCCAGAAAGATTCTGTTTATGCTGTGCCCTTAT 659

61 CCAGGAATTATCTTTACCAAAATCCAAAAAGAGAGCTCTCTCATATCATGCCCCACAT 120

120

660 TTTCCA-----CGAGGATGGAATAATTCCACACAATAATGAGGAACATTTG 707

121 TTCCCATCCAGTCAGTATCATTTCTGGAGAATTTCCTCAACTTAAAGATAGTCATCTTG 180

708 GGGCTGGTCCTGCCGCTCATCATGGTCACTCTGCTACTCGGGAATCCTGAAAACCCCTG 767

b  
GGGCTGGTGCACACTGTTCATCATCCTCCCAATCCCATAAACCAG  
||||| |||| | |||| | |||| | |||| |  
181

[illegible]

Y /68 CTT CGGTGTCGAAACGAGAAGAGGCATAGGCAGTGAGAGTCATCTTCAACCATG 827

828 ATGTTTACTTTCTCTTCTGGACTCCCCTATAACATTGTCAATTCTCTGAACACCTTCCAG 887

[illegible]

2 501 ATTGCTGACGCTTCTCTGAGGCTCCCTACACATCGTCTCTGAGCACCTTCCAG 360

Y 888 GAA<sup>T</sup>TCTTCGGCCTGAGT-AACTGTGAAAGCACCAAGTCAACTGGACCAAGCCACGAGGT 946

b 361 GAATTC TTTGGCTTGAATAAACTGCAGTGGCTCTAACAGGCTGGACCAAGCCATGCAGGT 420

Y 947 GACAGAGACTCTTGGGATGACTCACTGCTGCATCAATCCCATCATCTATGCCCTTCGTTGG 1006

[illegible]

421 GACAGAGACCCCTGGGGGATGACGCACCTGCTGCATCAACCCCATCATCTACGCCCTTCGTGGG 480

Downloaded from <http://ajph.org/> on November 10, 2014

```

RESULT 6
AA671573
LOCUS
DEFINITION
v104901.r2 Soares_mammary_gland_NBMGM Mus musculus cDNA clone
IMAGE:963216 5' similar to TR:G1322040 G1322040 C-C CHEMOKINE
RECEPTOR. ; mRNA sequence.
AA671573
AA671573.1 GI:2643652
EST.
house musculus
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 447)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:552008
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 397.
Location/Qualifiers
1..447
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:963216"
/clone_lib="Soares_mammary_gland_NBMGM"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/Note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
TGTWACCAATCTGAAGTGGGAGCGCGCAATGTTTTTTTTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
BASE COUNT 104 a 102 c 92 g 149 t
ORIGIN
Query Match 14.8%; Score 292.6; DB 9; Length 447;
Best Local Similarity 80.7%; Pred. No. 1.1e-70;
Matches 359; Conservative 0; Mismatches 74; Indels 12; Gaps 1;
QY 424 TATTACAGGGCTGATACATCGGTATTATTTGGCGGAATCTCTTCATCATCCCTCA 483
DB 2 TATTACAGGGCTCTATCATATGGTTATTTGGTGAATCTCTTCATATCCCTCA 61
QY 484 CAATCGATAGACTCTGGCTATTGTCTCATGCTGTGTTTAAAGCCAGCAGGTCA 543
DB 62 CAATTGATAGGACTTGGCTATTGCCATGCTGTGTTTAAAGTCAGACGGTCA 121
QY 544 CCTTTGGGGTGTGACAGTGTGATCACCTGGTTGGTGGCTGTGTTTGTCTGTCCAG 603

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DB 122 ACTTTGGGGTGATACAAAGTGTAGTCACTTGGGCGGTGCTGTGTTTGCCTCTCTCCAG 181
QY 604 GAATCATCTTTACTAAATGCCAGAAAGATTCTGTTTATGCTGTGGCCCTTATTTTC 663
DB 182 AAATAATCTTTTACCAGATCTCAGAAAGAGGTTTTCATTATACATGCACTCTCATTTTC 241
QY 664 CA-----CGAGGATGGAATAATTTCCACACAATAATAGGAAACATTTTGGGGC 711
DB 242 CACACATCAGTATCATTTCTGGAAGAGTTTCCAAACATTAAGATGGTCACTCTTGAGCC 301
QY 712 TGGTCTCCCGCTGCTCATCATGTCATCTGCTACTCGGGAATCCGAAACCCCTGCTTC 771
DB 302 TGATCTCGCTCTACTTGTCTGTCATCTGCTACTCAGGAATTTCCACACCCCTGTTTC 361
QY 772 GGTGTCGAAACAGAGAGAGGCATAGGCGAGTCAGATCATCTTTCCACATCATGATG 831
DB 362 GCTGTAGGAATGAGAAGAGGACAGCGGCTGTGAGGCTCATCTTTGCCATCATGATG 421
QY 832 TTTACTTTCTCTTCTGGACTCCCTA 856
DB 422 TCTACTTTCTCTTCTGGACTCCCTA 446
RESULT 7
BM917063
LOCUS
DEFINITION
BM917063
AGENCOURT_6702060 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5483554
5', mRNA sequence.
ACCESSION
BM917063
VERSION
BM917063.1 GI:19367442
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1074)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2011 row: g column: 11
High quality sequence stop: 718.
Location/Qualifiers
1..1074
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5483554"
/clone_lib="NIH_MGC_106"
/tissue_type="natural killer cells, cell line"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: blood; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 240 a 282 c 245 g 302 t 5 others
ORIGIN
Query Match 14.6%; Score 289; DB 14; Length 1074;
Best Local Similarity 61.8%; Pred. No. 1.5e-69;
Matches 517; Conservative 0; Mismatches 301; Indels 18; Gaps 3;

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[illegible]

RESULT 14  
BG182330  
LOCUS  
BG182330 884 bp mRNA linear EST 21-APR-2001  
RST1196 Athersys RAGE Library Homo sapiens cdna, mRNA sequence.  
DEFINITION  
ACCESSION

BASE COUNT	191 a	231 c	206 g	256 t
ORIGIN				
Query Match		11.9%	Score 235.2;	DB 12; Length 884;
Best Local Similarity		62.0%;	Pred. No. 1.7e-54;	

Matches	448;	Conservative	0;	Mismatches	253;	Indels	21;	Gaps	4;
Qy	141	ACCACCTTTTGTGATTAATGATTAGCGTCTCCCTGTGCATATAAATTTGACGTGAAGCAAAAT	200						
Db	53	ACCACATCTACTACTGATGTCGTGGCCCTGCTCTGTGAAAAAGCTGATACCGAGCAGCTG	112						
Qy	201	GGGGCCCAACTCCCTGCGCTCCGCTCTACTCGCTGTGTTCATCTTTGGTTTGTGGGCAAC	260						
Db	113	ATGGCCCAAGTTTGTGCCCCGCTCTACTCCCTGTGTTCACCTGTGGCCCTCTTGGCAAT	172						
Qy	261	ATGCTGGTCGTCATCTTTAAATAAATGCAAAAAGCTGAAGTCGTTTGACTGCACATTATAC	320						
Db	173	GTGCTGGTGTGATGATCTCATATAAATACAGGAGGCTCCGAATATAGCCACACATCAT	232						
Qy	321	CTGCTCAACCTGGCCATCTCTGATCTCTTTTCTTATTAATCTCTCCCAATTTGTGGGCTCAC	380						
Db	233	CTGCTCAACCTGGCCATTTGGGACCTCTCTCTCTCCCTTCCATTCTGGATCCAC	292						
Qy	381	TCTG- --CTGCAAATGAGTGGGTCTTTGGGAATGCATGTCGAAATTAATTCACAGGCTG	437						
Db	293	TATGTCAGGGGGCAATACTGGGTTTGGCCATGGCAATGTAAGTCCTCTCAGGGTTT	352						
Qy	438	TATCACATCGGTTATTTTGGCGGAATCTTCTTCATCATCCTCTCTGACAAATCGATAGATAC	497						
Db	353	TATCACACAGGCTTGTACAGCGAGATCTTTTTCATAATCTCTGCTGACAAATCGACAGTAC	412						
Qy	498	CTGGCTATTGTCATGCTGTGTTGCTTTAAAAGCCAGGACGGTCACTTTGGGGTGGTG	557						
Db	413	CTGGCCATTGTCATGCTGTGTTGGCTTTGCGCCCTTCGAGCCCGGACTCTACTTTTGGTGTCATC	472						
Qy	558	ACAAGTGTGATCACTCGTTGGTGGTGTGTTTGTCTCTGTCGCCAGGAATCATCTTTTACT	617						
Db	473	ACCAGCATCTGCACTGGGSCCTGGCAGTCTAGCAGCTCTTCTCTGAATTTATCTTCTAT	532						
Qy	618	AAATGCCAGAAAGAAATCTGTTTATGTCGTGGCCCTTATTTTCCAGAG- - - - -	669						
Db	533	GAGACTGAAGAGTGTGTTGAAGAGACTCTTTGCAAGTCTCTCTACCCAGAGGATACAGTA	592						
Qy	670	---GATGGAATAATTTCCACACAAATAATGAGGAACATTTTGGGCTGGTCTGCCGCTG	725						
Db	593	TATAGCTGGAGGATTTCCACATCTTGAGATGACCATCTCTGTCTCGTTCTCCCTCTG	652						
Qy	726	CTCATATGTCATCTGCTACTCGGGAATCTCTGAAACCCCTGCTCGGTGTGCGAAACGAG	785						
Db	653	CTCGTTATGGCCATCTGCTACACAGAAATCAT-CAAAACGCTGCTGGGTGCCAGTAAC	711						
Qy	786	AAGAAGAGGCATAGGGCAGTGGAGTCACTTCACCATCATGATGTTTACTTTCTCTTC	845						
Db	712	AAAGA- - - - -CAGGCCATCCGGCTCATTTTGTTCATCATGCGGCTGTTTATTTTTC	766						
Qy	846	TG 847							
Db	767	TG 768							
RESULT	15								
LOCUS	BF171452								
DEFINITION	PC12593 Myeloma (PCL) cDNA library Homo sapiens								
ACCESSION	BF171452								
VERSION	BF171452.1								
KEYWORDS	EST.								
SOURCE	human.								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
TITLE	Claudio J.O., Tang, H., Khan, E.M., Voralia, M., Li, Z., Cukerman, E.,								
JOURNAL	Francisco-Pabalan, O., Liew, C.C. and Stewart, A.K.								
COMMENT	The transcriptional phenotype of myeloma cells								
	Unpublished (2000)								
	Contact: A. Keith Stewart, M.D.								

TITLE The transcriptional phenotype of  
JOURNAL Unpublished (2000)  
COMMENT Contact: A. Keith Stewart, M.D.

Oncology Research  
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PCR Primers  
FORWARD: 5'-GCCAAGCTCGAAATTAACCCCTCACTAAAGG-3'  
BACKWARD: 5'-CCAGTGAATGTAAATAGGACTCACTATAGGCG-3'  
Seq primer: 5'-GAAATTAACCTCACTAAGG-3'

## FEATURES

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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Myeloma (PCL) CDNA library"  
/sex="male"  
/tissue\_type="Blood"  
/cell\_type="myeloma"  
/dev\_stage="Plasma cell leukemia"  
/note="Vector: Lambda Zap Express; Site\_1: EcoRI; Site\_2: XhoI; mRNA was purified from plasma cell leukemia patient's peripheral blood containing >95% myeloma. An oligo d(T)18 primer containing XhoI restriction site was used to prime first strand synthesis using M-MLV reverse transcriptase. To protect the cDNAs from XhoI digestion in subsequent cloning step, the nucleotide analogue 5-methyl-dCTP was added to the nucleotide mixture and [a-32P]dATP was added to monitor the quantity and quality of first strand synthesis. After second-strand synthesis and blunting of cDNA termini, EcoRI adapters were ligated, followed by kinase treatment and digestion with XhoI. The cDNAs were then size-fractionated using Sephacryl S-500 column and then ligated into EcoRI and XhoI digested Lambda Zap Express vector. The ligation product was packaged using Gigapack II packaging extract. The library had primary titre of approx. 1x10<sup>6</sup>. Clones from the primary library were randomly selected for single pass sequencing."

BASE COUNT 67 a 53 c 45 g 65 t  
ORIGIN

Query Match 11.6%; Score 230; DB 12; Length 230;  
Best Local Similarity 100.0%; Pred. No. 3e-53;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 1 GTCACCCCAATGCATATCCACATGTCCTCAGGGAATAATCCAGAAAAAAGCTGTGGGTAGAG 60  
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QY 1366 ACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAATGCCCTATTACCTTGTGCTA 1425  
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Db 61 ACTTTGACTCTCCAGAAAGCTCATCTCAGCTCCTGAAAAATGCCCTATTACCTTGTGCTA 120  
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QY 1426 ATCCCTCTTTTCTAGTCTTCAATAATTTCTTCACTCAATCTGATTTCTGTCATGTCCTTG 1485  
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Db 121 ATCCCTCTTTTCTAGTCTTCAATAATTTCTTCACTCAATCTGATTTCTGTCATGTCCTTG 180  
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QY 1486 AATCAAGGCCAGCTGGAGGTGAAGAGAGAAATGTGACAGGCACAGATG 1535  
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